

STTK Structure and Alignment of Protein Kinase Motif

FIG. 1A

STTK (929 a.a.)

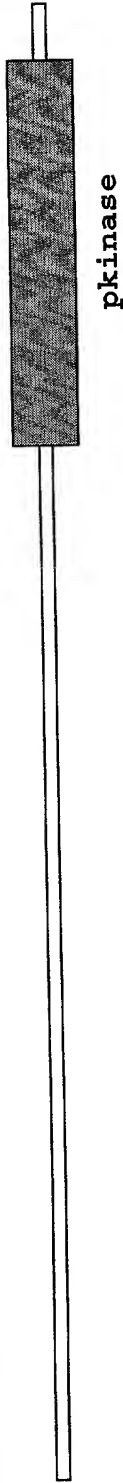


FIG. 1B

pkinese motif		10	20	30	40	50	60
consensus	*.....*.....*.....*.....					
STTK	1	YELGEKLGSGAFGKVYKGKHKD	---TGEIVAIKILK	---KRSLSKKKFLREIQILRR	53		
1DAW_A	652	pKLQELGRGQYGVVYLCDNWG	---GHFPCALKSVV	---PPDEKHWNLDLAL	EFHYMRS	703	
gi 125060	33	YEVVRKVGRGKYSEVFEGINVN	---NNEKCIKILK	---PVKKKK	---IKREIKILQN	81	
gi 125874	864	LKRIRDLGEGHFGKVELCRYDPedn	TGEQVAVKSLK	---PESGGNhiadL	KKEIEILRN	919	
	108	IQFIQKVGEAFSEVWEGWK	---GIHVAIKKLKi	igdeEQFKEr	---FIREVQNKK	159	
		70	80	90	100	110	120
consensus	*.....*.....*.....*.....*.....					
STTK	54	L-S-HPNIVRLLGVFE	---EDDH	---LYLVMEYMEGGDLFDYLRNGL	---LSE	97	
1DAW_A	704	LpK-HERLVDLHGSI	---DYNyggssiaVLLIMERL	-HRDLYTGLKAG	---LTL	751	
gi 125060	82	L-CgGPNIVKLLDIVRdqHKT	---PSLI FEYVNNTDFKVLYPTLT	---D	124		
gi 125874	920	L-Y-HENIVKYKIGICTedGGNG	---IKLIMEFLPSGLKEYLPKNKnk	---inL	965		
	160	G-N-HQNI VMFIGACY	---KP	---ACIITEYMAGGSLYNI LHNPNs	stpkvksF	206	

FIG. 1B pkinase motif (Continued)

		130	140	150	160	170	180
	*.....*.....*.....*.....*.....					
consensus	98	KEAKKIALQILRGLEYLHSGIVHRDLKPENILLDEN-GTVKIADFGLARKLESS-SYEK	155				
STTK	752	ETRLQIALDVVEGIRFLHSQGLVHRDIKLNVLDDKQ-NRAKITDLGFCK----	805				
1DAW_A	125	YDIRYIYELLKALDYCHSQGIMHRDVKPHNVIMIDHELKRLIDWGLAEFYHP----	181				
gi 125060	966	KQQLKYAVQICKGMDYLGSRQYVHRDLAARNVLVESE-HQVKIGDFGLTKAIEtdkeYYT	1024				
gi 125874	207	PLVLKMATDMALGLLHLHSITIVHRDLTSQNILLDEL-GNIKISDFGLSAEKSRegsmTM	265				
		190	200	210	220	230	240
	*.....*.....*.....*.....*.....					
consensus	156	LTTfVGTPPEYM-APEVLEG-RGYSSKVDVWSLGVILYELLTG-----	195				
STTK	806	SGSIVGTPiHM-APELFTG-K-YDnSVdVYAFGiLFWYICSGs-----	845				
1DAW_A	182	YNVRVASRYFK-GPELLVDlQDYDYSldMWslGCMFAGMIFRkepfyghdnhdqlvkia	240				
gi 125060	1025	VKDDRDSpVfWYAPECLMQ-SKFYIASDVWSFGVTLHELLTYcd-----	1067				
gi 125874	266	TNGGICNPRWR-PPELTkNlGHYSEKVDVYCFslVvWEILTG-----	306				
		250	260	270	280	290	300
	*.....*.....*.....*.....*.....					
consensus	196	---KLP--FPG-----IDPLEELFRiKERP-----RLRLPLPPNCSEELKDliKK	235				
STTK	846	---vKLPeaFER-----CASKDHLWNnVRRG-----A-RPERLPVFDEECWQLMEa	887				
1DAW_A	241	kvlgTDG--LNvYln-kyrIElDPQLEAlVGRHsrkpwLkFMNADNQHlVSPEaIDFLDK	297				
gi 125060	1068	--sdSSP--MALflkmigpTHGQMTVTRlVNTlk-----eGKRlPCPPNCpDEVYQlMRK	1118				
gi 125874	307	---EIP--FSD-----LDGSQRSAQVAYAG-----LRPPiPEYCDPElKlLLTQ	345				
		310	320				
	*.....*.....*.....					
consensus	236	CLNKDPEKRPTAKEILNHPWF	256				
STTK	888	CWDGDPLKRPllgivqpmLqg	908				
1DAW_A	298	LLRYDHQERLTAlEAMTHPYF	318				
gi 125060	1119	CwEFQPSNRtSFQNLIEGFea	1139				
gi 125874	346	CWeadPNDRPPFTYIVNKLke	366				

Structure of the STTK gene (Chr. 1q32.1)

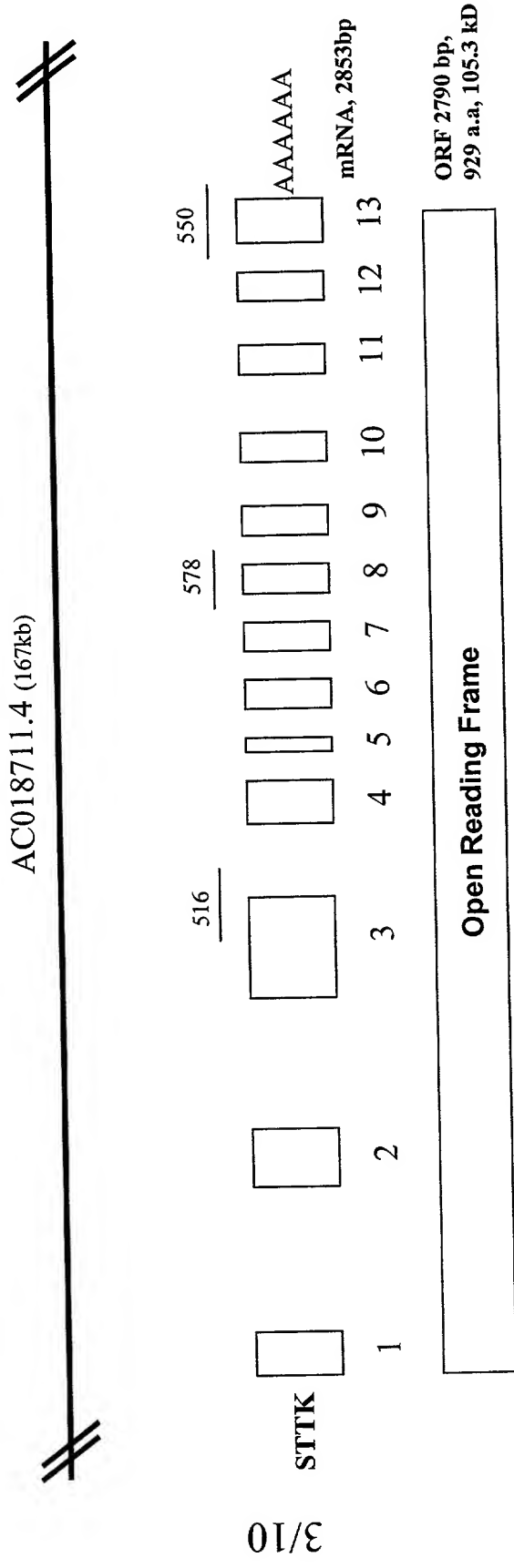


FIG. 2

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STTK

nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

M	E	G	D	G	V	P	W	G	S	E	P	V	13
ATG	GAG	GGC	GAC	GGG	GTG	CCA	TGG	GGC	AGC	GAG	CCC	GTC	39
S	G	P	G	P	G	G	G	G	M	I	R	E	26
TCG	GGT	CCC	GGC	CCC	GGC	GGC	GGC	GGA	ATG	ATC	CGC	GAG	78
L	C	R	G	F	G	R	Y	R	R	Y	L	G	39
CTG	TGC	CGG	GGC	TTC	GGC	CGC	TAC	CGC	CGC	TAC	CTG	GGA	117
R	L	R	Q	N	L	R	E	T	Q	K	F	F	52
CGG	CTG	CGA	CAG	AAC	CTG	CGC	GAG	ACC	CAG	AAG	TTC	TTC	156
R	D	I	K	C	S	H	N	H	T	C	L	S	65
CGC	GAC	ATC	AAG	TGC	TCC	CAC	AAC	CAC	ACT	TGT	CTC	TCC	195
S	L	T	G	G	G	G	A	E	R	G	P	A	78
TCC	CTC	ACG	GGC	GGC	GGC	GGG	GCC	GAG	CGC	GGC	CCT	GCA	234
G	D	V	A	E	T	G	L	Q	A	G	Q	L	91
GGC	GAT	GTC	GCC	GAA	ACC	GGG	CTG	CAG	GCG	GGC	CAA	CTG	273
S	C	I	S	F	P	P	K	E	E	K	Y	L	104
AGC	TGC	ATT	TCC	TTC	CCA	CCT	AAG	GAA	GAG	AAG	TAC	CTC	312
Q	Q	I	V	D	C	L	P	C	I	L	I	L	117
CAG	CAG	ATT	GTG	GAC	TGC	CTC	CCT	TGC	ATA	CTG	ATC	CTC	351
G	Q	D	C	N	V	K	C	Q	L	L	N	L	130
GGC	CAG	GAT	TGT	AAC	GTC	AAG	TGC	CAG	CTG	TTG	AAT	CTG	390
L	L	G	V	Q	V	L	P	T	T	K	L	G	143
CTG	TTG	GGG	GTG	CAG	GTG	CTT	CCC	ACC	ACC	AAG	CTG	GGC	429

FIG. 3

S	E	E	S	C	K	L	R	R	L	R	F	T	156
AGT	GAG	GAG	AGC	TGT	AAG	CTT	CGG	CGC	CTC	CGC	TTC	ACC	468
Y	G	T	Q	T	R	V	S	L	A	L	P	G	169
TAT	GGG	ACT	CAG	ACT	CGG	GTC	AGC	CTG	GCG	CTC	CCT	GGA	507
Q	Y	E	L	V	H	T	L	V	A	H	Q	G	182
CAG	TAT	GAA	CTA	GTG	CAC	ACG	CTG	GTT	GCT	CAT	CAG	GGC	546
N	W	E	T	I	P	E	E	D	L	E	V	Q	195
AAC	TGG	GAG	ACC	ATC	CCT	GAG	GAG	GAT	CTG	GAG	GTC	CAA	585
E	N	N	E	D	A	A	H	V	L	A	E	L	208
GAG	AAC	AAT	GAG	GAT	GCT	GCT	CAT	GTT	TTA	GCG	GAA	CTG	624
E	V	T	M	H	H	A	L	L	Q	E	V	D	221
GAG	GTA	ACG	ATG	CAC	CAT	GCT	CTC	TTA	CAG	GAA	GTG	GAC	663
V	V	V	A	P	C	Q	G	L	R	P	T	V	234
GTT	GTG	GTA	GCA	CCA	TGC	CAA	GGC	CTC	CGG	CCC	ACA	GTG	702
D	V	L	G	D	L	V	N	D	F	L	P	V	247
GAT	GTT	CTG	GGT	GAC	TTG	GTG	AAT	GAT	TTC	TTG	CCT	GTG	741
I	T	Y	A	L	H	K	D	E	L	S	E	R	260
ATA	ACC	TAT	GCA	CTC	CAC	AAA	GAT	GAA	CTC	TCT	GAG	AGG	780
D	E	Q	E	L	Q	E	I	R	K	Y	F	S	273
GAT	GAG	CAA	GAG	CTT	CAG	GAA	ATC	CGA	AAG	TAT	TTC	TCC	819
F	P	V	F	F	F	K	V	P	K	L	G	S	286
TTT	CCT	GTA	TTC	TTT	TTC	AAA	GTG	CCG	AAA	CTG	GGC	TCG	858
E	I	I	D	S	S	T	R	R	M	E	S	E	299
GAG	ATA	ATA	GAC	TCC	TCA	ACC	AGG	AGA	ATG	GAG	AGC	GAA	897
R	S	P	L	Y	R	Q	L	I	D	L	G	Y	312
AGA	TCA	CCG	CTT	TAT	CGC	CAG	CTA	ATT	GAC	CTG	GGC	TAT	936
L	S	S	S	H	W	N	C	G	A	P	G	Q	325
CTG	AGC	AGC	AGT	CAC	TGG	AAC	TGT	GGG	GCT	CCT	GGC	CAG	975

FIG. 3

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D	T	K	A	Q	S	M	L	V	E	Q	S	E	338
GAT	ACT	AAA	GCT	CAG	AGC	ATG	TTG	GTG	GAA	CAG	AGT	GAA	1014
K	L	R	H	L	S	T	F	S	H	Q	V	L	351
AAG	CTG	AGA	CAC	TTG	AGC	ACA	TTT	TCT	CAC	CAG	GTG	TTA	1053
Q	T	R	L	V	D	A	A	K	A	L	N	L	364
CAG	ACT	CGC	CTG	GTG	GAT	GCA	GCC	AAG	GCC	CTG	AAC	CTG	1092
V	H	C	H	C	L	D	I	F	I	N	Q	A	377
GTG	CAC	TGC	CAC	TGC	CTT	GAC	ATC	TTT	ATT	AAC	CAG	GCA	1131
F	D	M	Q	R	D	L	Q	I	T	P	K	R	390
TTT	GAC	ATG	CAG	CGG	GAC	CTG	CAG	ATC	ACT	CCC	AAA	CGT	1170
L	E	Y	T	R	K	K	E	N	E	L	Y	E	403
CTG	GAA	TAT	ACT	CGA	AAA	AAG	GAG	AAT	GAG	TTG	TAT	GAA	1209
S	L	M	N	I	A	N	R	K	Q	E	E	M	416
TCA	TTG	ATG	AAT	ATT	GCC	AAC	CGA	AAG	CAG	GAG	GAA	ATG	1248
K	D	M	I	V	E	T	L	N	T	M	K	E	429
AAG	GAT	ATG	ATT	GTT	GAG	ACA	CTT	AAT	ACC	ATG	AAG	GAG	1287
E	L	L	D	D	A	T	N	M	E	F	K	D	442
GAA	CTT	CTG	GAT	GAT	GCT	ACT	AAC	ATG	GAG	TTT	AAA	GAC	1326
V	I	V	P	E	N	G	E	P	V	G	T	R	455
GTC	ATT	GTC	CCT	GAG	AAT	GGA	GAA	CCA	GTA	GGC	ACC	AGA	1365
E	I	K	C	C	I	R	Q	I	Q	E	L	I	468
GAG	ATC	AAA	TGC	TGC	ATC	CGA	CAG	ATC	CAG	GAA	CTC	ATC	1404
I	S	R	L	N	Q	A	V	A	N	K	L	I	481
ATC	TCC	CGA	CTT	AAT	CAG	GCA	GTG	GCT	AAT	AAG	CTG	ATC	1443
S	S	V	D	Y	L	R	E	S	F	V	G	T	494
AGC	TCA	GTG	GAT	TAC	CTG	AGG	GAA	AGC	TTC	GTC	GGA	ACC	1482
L	E	R	C	L	Q	S	L	E	K	S	Q	D	507
CTG	GAA	CGA	TGT	CTG	CAG	AGC	CTG	GAG	AAG	TCT	CAG	GAT	1521

FIG. 3

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V	S	V	H	I	T	S	N	Y	L	K	Q	I	520
GTC	TCA	GTT	CAC	ATC	ACC	AGT	AAT	TAT	CTC	AAA	CAG	ATC	1560
L	N	A	A	Y	H	V	E	V	T	F	H	S	533
TTA	AAT	GCT	GCC	TAT	CAT	GTT	GAA	GTC	ACG	TTT	CAC	TCA	1599
G	S	S	V	T	R	M	L	W	E	Q	I	K	546
GGG	TCG	TCA	GTT	ACA	AGG	ATG	CTA	TGG	GAG	CAA	ATC	AAA	1638
Q	I	I	Q	R	I	T	W	V	S	P	P	A	559
CAG	ATC	ATC	CAG	CGC	ATC	ACA	TGG	GTG	AGC	CCA	CCT	GCC	1677
I	T	L	E	W	K	R	K	V	A	Q	E	A	572
ATC	ACT	CTG	GAA	TGG	AAG	AGG	AAG	GTG	GCC	CAG	GAA	GCC	1716
I	E	S	L	S	A	S	K	L	A	K	S	I	585
ATT	GAG	AGC	CTC	AGC	GCC	TCC	AAA	TTG	GCT	AAG	AGC	ATT	1755
C	S	Q	F	R	T	R	L	N	S	S	H	E	598
TGC	AGC	CAA	TTC	CGG	ACT	CGG	CTC	AAT	AGT	TCC	CAC	GAG	1794
A	F	A	A	S	L	R	Q	L	E	A	G	H	611
GCT	TTT	GCA	GCC	TCC	TTG	CGG	CAG	CTG	GAA	GCT	GGC	CAC	1833
S	G	R	L	E	K	T	E	D	L	W	L	R	624
TCA	GGC	CGG	TTA	GAG	AAA	ACG	GAA	GAT	CTA	TGG	CTG	AGG	1872
V	R	K	D	H	A	P	R	L	A	R	L	S	637
GTT	CGG	AAA	GAT	CAT	GCT	CCC	CGC	CTG	GCC	CGC	CTT	TCT	1911
L	E	S	R	S	L	Q	D	V	L	L	H	R	650
CTG	GAA	AGC	CGT	TCT	TTA	CAG	GAT	GTC	TTG	CTT	CAT	CGT	1950
K	P	K	L	G	Q	E	L	G	R	G	Q	Y	663
AAA	CCT	AAA	CTG	GGA	CAG	GAA	CTG	GGC	CGG	GGC	CAG	TAT	1989
G	V	V	Y	L	C	D	N	W	G	G	H	F	676
GGT	GTG	GTA	TAC	CTG	TGT	GAC	AAC	TGG	GGA	GGA	CAC	TTC	2028
P	C	A	L	K	S	V	V	P	P	D	E	K	689
CCT	TGT	GCC	CTC	AAA	TCA	GTT	GTC	CCT	CCA	GAT	GAG	AAG	2067

FIG. 3

H	W	N	D	L	A	L	E	F	H	Y	M	R	702
CAC	TGG	AAT	GAT	CTG	GCT	TTG	GAA	TTT	CAC	TAT	ATG	AGG	2106
S	L	P	K	H	E	R	L	V	D	L	H	G	715
TCT	CTG	CCG	AAG	CAT	GAG	CGA	TTG	GTG	GAT	CTC	CAT	GGT	2145
S	V	I	D	Y	N	Y	G	G	G	S	S	I	728
TCA	GTC	ATT	GAC	TAC	AAC	TAT	GGT	GGT	GGC	TCC	AGC	ATT	2184
A	V	L	L	I	M	E	R	L	H	R	D	L	741
GCT	GTG	CTC	CTC	ATT	ATG	GAG	CGG	CTA	CAC	CGG	GAT	CTC	2223
Y	T	G	L	K	A	G	L	T	L	E	T	R	754
TAC	ACA	GGG	CTG	AAG	GCT	GGG	CTG	ACC	CTG	GAG	ACA	CGT	2262
L	Q	I	A	L	D	V	V	E	G	I	R	F	767
TTG	CAG	ATA	GCA	CTA	GAT	GTG	GTG	GAG	GGA	ATC	CGC	TTC	2301
L	H	S	Q	G	L	V	H	R	D	I	K	L	780
CTG	CAC	AGC	CAG	GGA	CTT	GTC	CAT	CGT	GAT	ATC	AAA	CTG	2340
K	N	V	L	L	D	K	Q	N	R	A	K	I	793
AAA	AAT	GTG	CTG	CTG	GAT	AAG	CAG	AAC	CGT	GCC	AAG	ATC	2379
T	D	L	G	F	C	K	P	E	A	M	M	S	806
ACT	GAC	TTA	GGA	TTC	TGC	AAG	CCA	GAG	GCC	ATG	ATG	TCA	2418
G	S	I	V	G	T	P	I	H	M	A	P	E	819
GGC	AGC	ATT	GTG	GGG	ACA	CCA	ATC	CAT	ATG	GCC	CCT	GAA	2457
L	F	T	G	K	Y	D	N	S	V	D	V	Y	832
CTT	TTC	ACA	GGG	AAG	TAC	GAT	AAT	TCC	GTG	GAT	GTC	TAC	2496
A	F	G	I	L	F	W	Y	I	C	S	G	S	845
GCT	TTT	GGA	ATT	CTT	TTC	TGG	TAT	ATC	TGC	TCA	GGC	TCT	2535
V	K	L	P	E	A	F	E	R	C	A	S	K	858
GTC	AAG	CTC	CCT	GAG	GCA	TTT	GAG	AGG	TGT	GCT	AGC	AAA	2574
D	H	L	W	N	N	V	R	R	G	A	R	P	871
GAC	CAT	CTC	TGG	AAC	AAT	GTG	CGG	AGG	GGG	GCT	CGC	CCA	2613

FIG. 3

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E	R	L	P	V	F	D	E	E	C	W	Q	L	884
GAA	CGT	CTT	CCT	GTG	TTT	GAT	GAG	GAG	TGC	TGG	CAG	TTG	2652
M	E	A	C	W	D	G	D	P	L	K	R	P	897
ATG	GAA	GCC	TGT	TGG	GAT	GGC	GAC	CCC	TTG	AAG	AGG	CCT	2691
L	L	G	I	V	Q	P	M	L	Q	G	I	M	910
CTC	TTG	GGC	ATT	GTC	CAG	CCC	ATG	CTC	CAG	GGC	ATC	ATG	2730
N	R	L	C	K	S	N	S	E	Q	P	N	R	923
AAT	CGG	CTC	TGC	AAG	TCC	AAT	TCT	GAG	CAG	CCA	AAC	AGA	2769
G	L	D	D	S	T	*							930
GGA	CTA	GAT	GAT	TCT	ACT	TGA	AAGCAAAGACCTTTCTCTTTCAC						2813
TCTCTAGTTATTTTCCTTCCCCCTCACCTTTTGGCCATGGG													2853

FIG. 3

Tissue Expression Profile of Human STTK

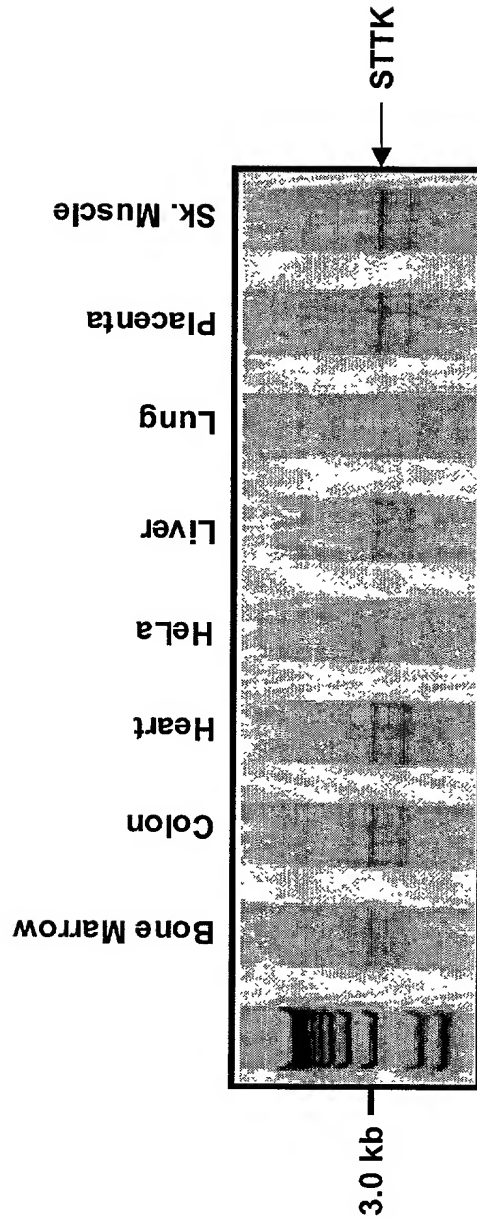


FIG. 4